

RECEIVED

SEP 20 2002

TECH CENTER 1600/2900

APPROVED	FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		



1/5

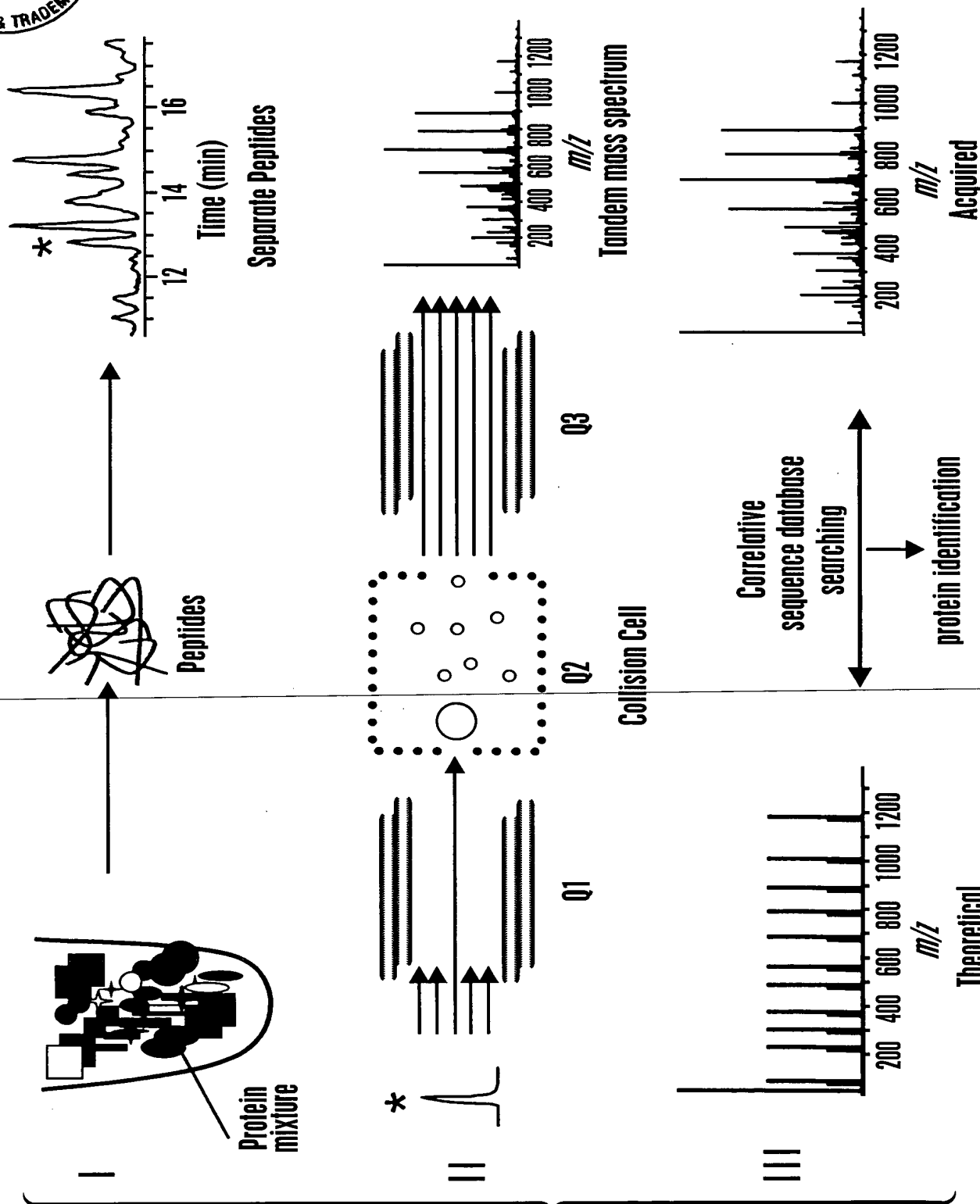
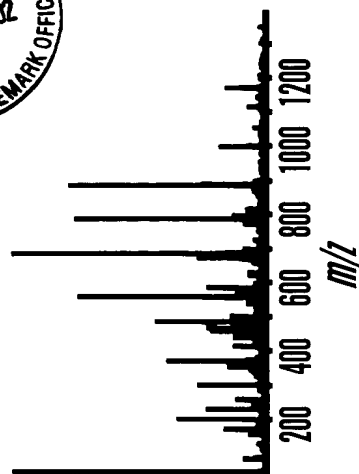


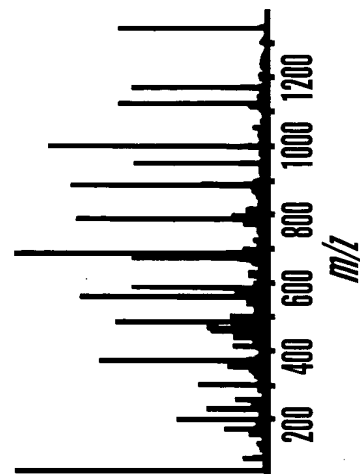
Figure 1

2/5

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DP/AFSMA		



Mass spectrum consists of fragment ions specific to selected parent ion.



Mass spectrum consists of fragment ions from multiple parent ions.

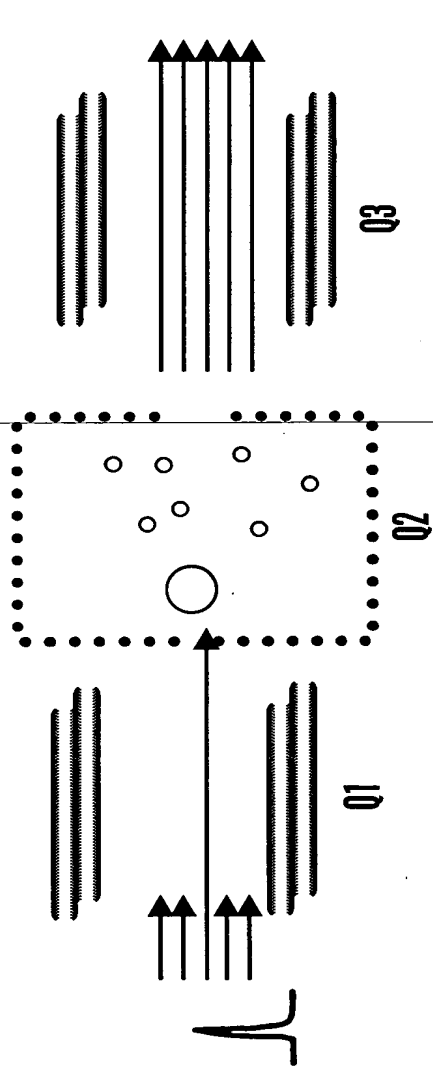


Fig. 2A

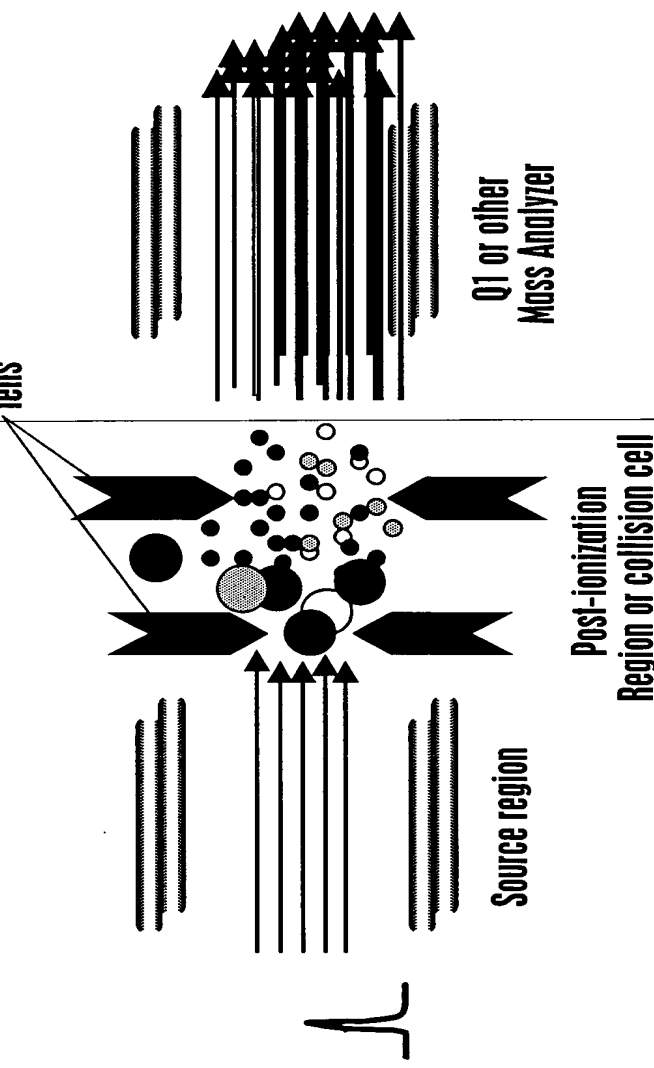


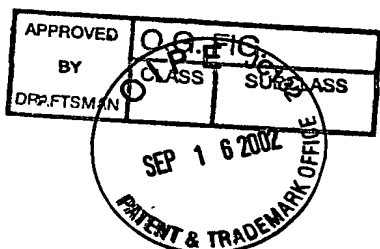
Fig. 2B

RECEIVED

SEP 20 2002

TECH CENTER 1600/2900

3/5

**Growth Condition 1**

1a) Grow Cells or Harvest Tissue from Biopsy or Collect serum or spinal fluid, etc.

Growth Condition 2

1b) Grow Cells or Harvest Tissue from Biopsy or Collect serum or spinal fluid, etc.

State 1

2) Harvest Proteins & Label separately with Isotopically distinct ICAT reagents such that State 1 & 2 can be distinguished after mixing.

State 2**State 1****State 2**

3) Combine labeled Proteins from States 1 & 2.

1 + 2

- 4) Fractionate proteins by molecular weight.
- 5) Digest proteins to peptides (e.g. using Trypsin).
- 6) Separate peptides by ion exchange and collect fractions.
- 7) Purify each ion fraction by affinity chromatography.
- 8) Analyze each affinity chromatography fraction by LC/MS or MALDI-MS after LC fractionation.

9) Use annotated peptide tag database to identify proteins and quantitate relative abundance between states.

Figure 3

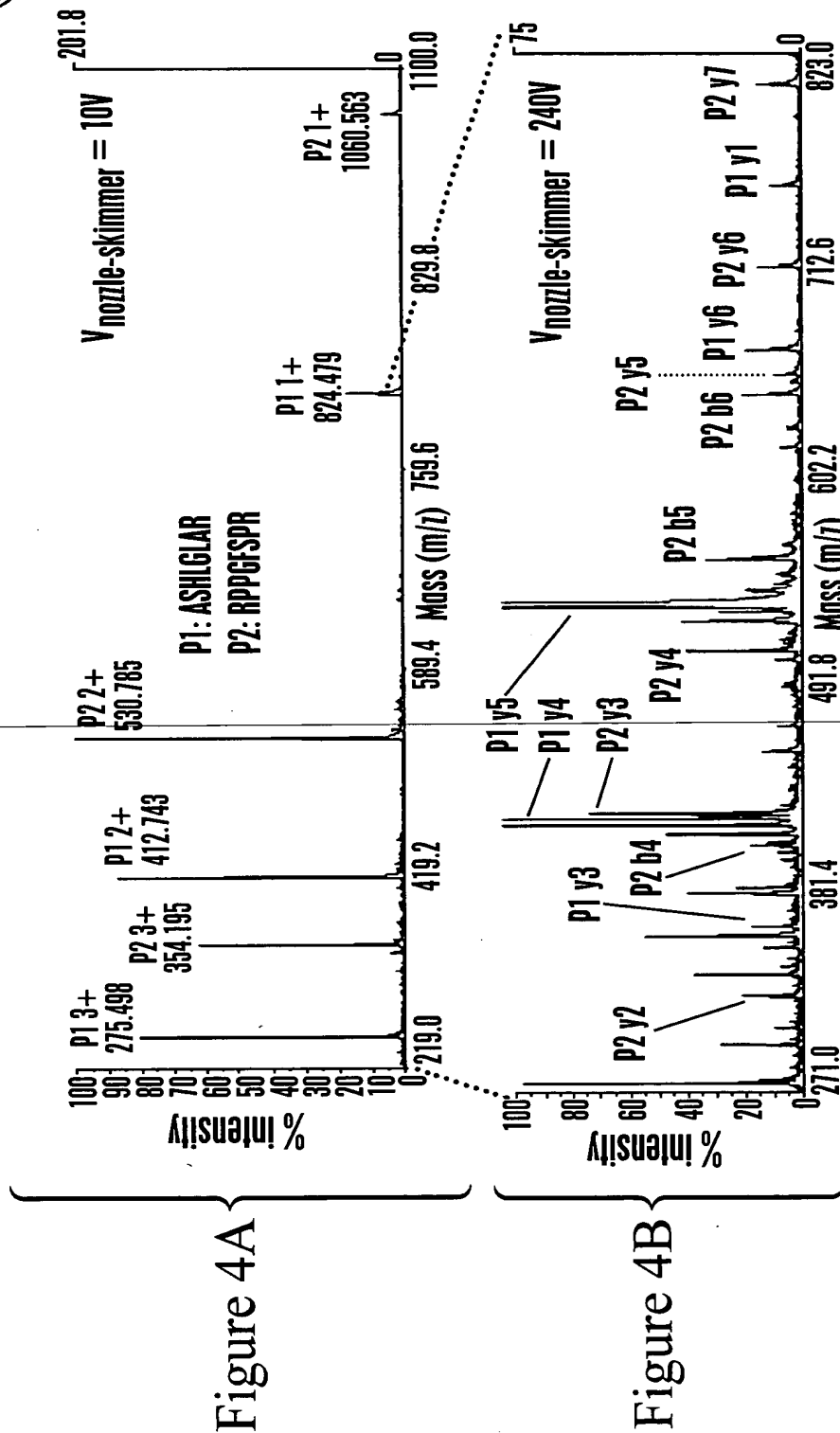
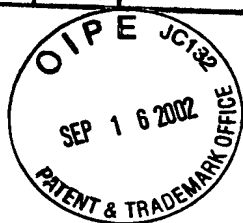
RECEIVED

SEP 20 2002

TECH CENTER 1600/2900

4/5

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DP,FTSMAN		



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Title: Rapid and Quantitative Proteome Analysis and Related Methods
 Inventor: David R. Goodlett
 Serial No.: 09/748,783 (Confirmation No. 3333)
 Filing Date: December 26, 2000
 Attorney Docket: P-IS 4369
 USPTO Customer No. 23601 (858-535-9001)

RECEIVED

SEP 20 2002

TECH CENTER 1600/2900

5/5

Human protein database:

60,884 sequence entries

Fragment ion masses used for analysis:

710.385
 753.435
 807.374
 886.402
 904.451
 1001.564

 Bradykinin RPPGFSPFR MH+ 1060.5676

at 10 PPM, 144 tryptic peptides match

13 matches using fragment ion constraint:

ACISEILPSK
 GVRYSFGFK
 RANLISQCR
 RCGLPSSGKR
 RDITLEASR
 RERETLEK
 RLTEEERK
 RLVEVDSSR
 RNLLDHR
 RPAAQPGAR
 RPPGFSPFR **
 RPQTATASTK
 RRPSAYQAL

 ASHLGLAR MH+ 824.4739

at 10 PPM, 57 tryptic peptides match

12 matches using fragment ion constraint:

ACYIKVK
 ADPLPRR
 AFVAFAAK
 AFVFGRK
 AHAEIRK
 AHEAKIR
 ALEAHKR
 ALQFFAK
 AMAIYKK
 APDPRLR
 ASHLGLAR **
 AVAGHLTR

Figure 4C